

02-20-03

IN THE UNITED STATES PATENT AND TRADEMARK OFFICE

plicant: Ramnarayan et al.

Serial No.: 09/704,362

Confirmation No.: 4748

Filed:

November 1, 2000

For:

USE OF COMPUTATIONALLY DERIVED PROTEIN STRUCTURES OF GENETIC

POLYMORPHISMS IN

PHARMACOGENOMICS FOR DRUG DESIGN AND CLINICAL APPLICATIONS

Art Unit:

1631

U.S. Patent and Trademark Office

Examiner:

P.O. Box 2327

Commissioner for Patents

Arlington, VA 22202

Brusca, J.

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Sir:

Transmitted herewith are an Amendment and Response responsive to the Office Action mailed August 13, 2002, a Supplemental Information Disclosure Statement (SIDS); Form PTO-1449 (1 page), cited references, and a check for \$645 for a three-month extension of time (\$465) by small entity and the SIDS filing fee (\$180) for filing in connection with the above-identified application. If a Petition for extension of time is needed, this paper is to be considered such Petition.

The Commissioner is hereby authorized to charge this fee and any fees, including the fee for X the extension of time, if the above noted amount is incorrect, that may be due in connection with this and the attached papers or with this application during its entire pendency to Deposit Account No. 50-1213 (or Deposit Account No. 08-1641). A duplicate of this sheet is enclosed.

02/25/2003 CNGUYEN 00000016 09704362

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Respectfully submitted, HELLER EHRMAN WHITE & MOAULIFFE LLP

By:

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ATTACHMENTS TO AMENDMENT RESPONSIVE TO OFFICE ACTION

The following attachments are provided:

- (1) A Supplemental Information Disclosure Statement and Form PTO-1449(1 page) making of record art cited in the Response; and
 - (2) Copies of the following documents

Osguthorpe, "Improved Ab Initio Predictions with a Simplified, Flexible Geometry Model," Proteins: Structure, Function, and Genetics Suppl 3 (November 9, 1999) 186-193;

Westhead and Thornton "Protein structure prediction," Curr Opin in Biotechnology (1998) 9:383-389, ;

Eisenhaber *et al.* "Protein structure prediction: recognition of primary, secondary, and tertiary structural features from amino acid sequence," Critical Rev. in Biochem and Mol. Biol. (1995) 30:1-94;

Jones, "Successful *ab initio* prediction of the tertiary structure of NK-Lysin using multiple sequences and recognized supersecondary structural motifs," Proteins: Structure, function, and Genetics, Suppl 1 (1997) 185-191; U.S.S.N. 09/704,362 RAMNARAYAN *ET AL.* ATTACHMENTS TO AMENDMENT

Samudrala *et al.*, "Ab initio protein structure prediction using a combined hierarchical approach," Proteins: Structure, function, and Genetics Suppl 3 (1999) 194-198;

Dunbrack *et al.* "Meeting review: the Second Meeting on the Critical Assessment of Techniques for Protein Structure Prediction (CASP2), Asilomar, California, December 13-16, 1996," Folding and Design (1997) R27-R42; and de Dios *et al.* "Secondary and Tertiary Structural Effects on Protein NMR Chemical Shifts: An ab Initio Approach," Science (1993) 260:1491-1496.

U.S. Patent No. 5,736,509 (April 7, 1998)